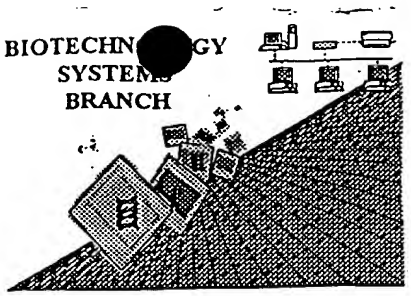
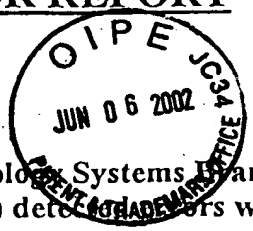
Rerun

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/647,140

Source: PCT/09

Date Processed by STIC: 6/18/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Please mail this Raw Sequence Listing Error Report with the 905.

Raw Sequence Listing Error Summary

ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/647,140

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PCT09

RAW SEQUENCE LISTING DATE: 06/18/2001
PATENT APPLICATION: US/09/647,140 TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt
Output Set: N:\CRF3\06182001\I647140.raw

Does Not Comply
Corrected Diskette Needed
p.6

```
  3 <110> APPLICANT: Fox Chase Cancer Center
  4       Kruh, Gary D.
  5       Lee, Kun
  6       Belinsky, Martin G.
  7       Bain, Lisa J.
  9 <120> TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
 10       Nucleic Acids and Methods of Use Thereof
 12 <130> FILE REFERENCE: FCCC 98-02
 14 <140> CURRENT APPLICATION NUMBER: 09/647,140
--> 15 <141> CURRENT FILING DATE: 2001-05-21
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/06644
 18 <151> PRIOR FILING DATE: 1999-03-26
 20 <150> PRIOR APPLICATION NUMBER: 60/079,759
 21 <151> PRIOR FILING DATE: 1998-03-27
 23 <150> PRIOR APPLICATION NUMBER: 60/095,153
 24 <151> PRIOR FILING DATE: 1998-08-03
 26 <160> NUMBER OF SEQ ID NOS: 18
 28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 4231
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
 36 <400> SEQUENCE: 1
 37  ggacaggcgt ggcggccgga gccccagcat ccctgcttga ggtccaggag cggagcccgc      60
 38  ggccaccgcc gcctgatcag cgcgaccccg gcccgcgccc gccccgcccg gcaagatgct     120
 39  gcccgtgtac caggaggtga agcccaaccc gctgcaggac gcgaacatct gctcacgcgt     180
 40  gttcttctgg tggctcaatc ccttgtttaa aattggccat aaacggagat tagaggaaga     240
 41  tgatatgtat tcagtgctgc cagaagaccg ctcacagcac cttggagagg agttgcaagg     300
 42  gttctgggat aaagaagttt taagagctga gaatgacgca cagaagcctt ctttaacaag     360
 43  agcaatcata aagtgttact ggaaatctta tttagttttg ggaattttta cgttaattga     420
 44  ggaaagtgcc aaagtaatcc agcccatatt tttgggaaaa attattaatt attttgaaaa     480
 45  ttatgatccc atggattctg tggctttgaa cacagcgtac gcctatgcca cggtgctgac     540
 46  tttttgcacg ctcattttgg ctatactgca tcacttatat ttttatcacg ttcagtgtgc     600
 47  tgggatgagg ttacgagtag ccatgtgcca tatgatttat cggaaggcac ttcgtcttag     660
 48  taacatggcc atggggaaga caaccacagg ccagatagtc aatctgctgt ccaatgatgt     720
 49  gaacaagttt gatcaggtga cagtgttctt acacttcctg tgggcaggac cactgcaggc     780
 50  gatcgcagtg actgccctac tctggatgga gataggaata tcgtgccttg ctgggatggc     840
 51  agttctaatc attctcctgc ccttgaaaag ctgttttggg aagttgttct catcactgag     900
 52  gagtaaaact gcaactttca cggatgccag gatcaggacc atgaatgaag ttataactgg     960
 53  tataaggata ataaaaatgt acgcctggga aaagtcattt tcaaatctta ttaccaattt    1020
 54  gagaaagaag gagatttcca agattctgag aagttcctgc ctcaggggga tgaatttggc    1080
 55  ttcgtttttc agtgcaagca aaatcatcgt gtttgtgacc ttcaccacct acgtgctcct    1140
 56  cggcagtgtg atcacagcca gccgcgtgtt cgtggcagtg acgctgtatg gggctgtgcg    1200
 57  gctgacggtt accctcttct tcccctcagc cattgagagg gtgtcagagg caatcgtcag    1260
 58  catccgaaga atccagacct ttttgctact tgatgagata tcacagcgca accgtcagct    1320
 59  gccgtcagat ggtaaaaaga tggtgcatgt gcaggatttt actgcttttt gggataaggc    1380
 60  atcagagacc ccaactctac aaggcctttc ctttactgtc agacctggcg aattgttagc    1440
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RAW SEQUENCE LISTING DATE: 06/18/2001
PATENT APPLICATION: US/09/647,140 TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt
Output Set: N:\CRF3\06182001\I647140.raw

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 61  tgtggtcggc cccgtgggag cagggaagtc atcactgtta agtgccgtgc tcggggaatt    1500
 62  ggccccaagt cacgggctgg tcagcgtgca tggaagaatt gcctatgtgt ctcagcagcc    1560
 63  ctgggtgttc tcgggaactc tgaggagtaa tattttattt gggaagaaat atgaaaagga    1620
 64  acgatatgaa aaagtcataa aggcttgtgc tctgaaaaag gatttacagc tgttggagga    1680
 65  tggtgatctg actgtgatag gagatcgggg aaccacgctg agtggagggc agaaagcacg    1740
 66  ggtaaacctt gcaagagcag tgtatcaaga tgctgacatc tatctcctgg acgatcctct    1800
 67  cagtgcagta gatgcggaag ttagcagaca cttgttcgaa ctgtgtattt gtcaaatttt    1860
 68  gcatgagaag atcacaattt tagtgactca tcagttgcag tacctcaaag ctgcaagtca    1920
 69  gattctgata ttgaaagatg gtaaaatggt gcagaagggg acttacactg agttcctaaa    1980
 70  atctggtata gattttggct ccctttttaaa gaaggataat gaggaaagtg aacaacctcc    2040
 71  agttccagga actcccacac taaggaatcg taccttctca gagtcttcgg tttggtctca    2100
 72  acaatcttct agaccctcct tgaaagatgg tgctctggag agccaagata cagagaatgt    2160
 73  cccagttaca ctatcagagg agaaccgttc tgaaggaaaa gttggttttc aggcctataa    2220
 74  gaattacttc agagctggtg ctcactggat tgtcttcatt ttccttattc tcctaaacac    2280
 75  tgcagctcag gttgcctatg tgcttcaaga ttggtggctt tcatactggg caaacaaaca    2340
 76  aagtatgcta aatgtcactg taaatggagg aggaaatgta accgagaagc tagatcttaa    2400
 77  ctggtactta ggaatttatt caggtttaac tgtagctacc gttctttttg gcatagcaag    2460
 78  atctctattg gtattctacg tccttgttaa ctcttcacaa actttgcaca acaaaatgtt    2520
 79  tgagtcaatt ctgaaagctc cggtattatt ctttgataga aatccaatag gaagaatttt    2580
 80  aaatcgtttc tccaaagaca ttggacactt ggatgatttg ctgccgctga cgtttttaga    2640
 81  tttcatccag acattgctac aagtggttgg tgtggtctct gtggctgtgg ccgtgattcc    2700
 82  ttggatcgca ataccccttgg ttccccttgg aatcattttc atttttcttc ggcgatattt    2760
 83  tttggaaacg tcaagagatg tgaagcgcct ggaatctaca actcggagtc cagtgttttc    2820
 84  ccacttgtca tcttctctcc aggggctctg gaccatccgg gcatacaaag cagaagagag    2880
 85  gtgtcaggaa ctgtttgatg cacaccagga tttacattca gaggcttggt tcttgttttt    2940
 86  gacaacgtcc cgctggttcg ccgtccgtct ggatgccatc tgtgccatgt ttgtcatcat    3000
 87  cgttgccttt gggtccctga ttctggcaaa aactctggat gccgggcagg ttggtttggc    3060
 88  actgtcctat gccctcacgc tcatggggat gtttcagtgg tgtgttcgac aaagtgctga    3120
 89  agttgagaat atgatgatct cagtagaaag ggtcattgaa tacacagacc ttgaaaaaga    3180
 90  agcaccttgg gaatatcaga aacgcccacc accagcctgg ccccatgaag gagtgataat    3240
 91  ctttgacaat gtgaacttca tgtacagtcc aggtgggcct ctggtactga agcatctgac    3300
 92  agcactcatt aaatcacaag aaaaggttgg cattgtggga agaaccggag ctggaaaaag    3360
 93  ttccctcatc tcagcccttt ttagattgtc agaacccgaa ggtaaaattt ggattgataa    3420
 94  gatcttgaca actgaaattg gacttcacga tttaaggaag aaaatgtcaa tcatacctca    3480
 95  ggaacctgtt ttgttcactg gaacaatgag gaaaaacctg gatcccttta aggagcacac    3540
 96  ggatgaggaa ctgtggaatg ccttacaaga ggtacaactt aaagaaacca ttgaagatct    3600
 97  tcctggtaaa atggatactg aattagcaga atcaggatcc aattttagtg ttggacaaag    3660
 98  acaactggtg tgccttgcca gggcaattct caggaaaaat cagatattga ttattgatga    3720
 99  agcgacggca aatgtggatc caagaactga tgagttaata caaaaaaaaa tccgggagaa    3780
100   atttgcccac tgcaccgtgc taaccattgc acacagattg aacaccatta ttgacagcga    3840
101   caagataatg gttttagatt caggaagact gaaagaatat gatgagccgt atgttttgct    3900
102   gcaaaataaa gagagcctat tttacaagat ggtgcaacaa ctgggcaagg cagaagccgc    3960
103   tgccctcact gaaacagcaa aacaggtata cttcaaaaga aattatccac atattggtca    4020
104   cactgaccac atggttacaa acacttccaa tggacagccc tcgaccttaa ctattttcga    4080
105   gacagcactg tgaatccaac caaaatgtca agtccgttcc gaaggcattt tccactagtt    4140
106   tttggactat gtaaaccaca ttgtactttt ttttactttg gcaacaaata tttatacata    4200
107   caagatgcta gttcatttga atatttctcc c                                  4231
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 1325
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RAW SEQUENCE LISTING DATE: 06/18/2001
PATENT APPLICATION: US/09/647,140 TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt
Output Set: N:\CRF3\06182001\I647140.raw

<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 2

Met	Leu	Pro	Val	Tyr	Gln	Glu	Val	Lys	Pro	Asn	Pro	Leu	Gln	Asp	Ala
1				5					10					15	
Asn	Ile	Cys	Ser	Arg	Val	Phe	Phe	Trp	Trp	Leu	Asn	Pro	Leu	Phe	Lys
			20					25					30		
Ile	Gly	His	Lys	Arg	Arg	Leu	Glu	Glu	Asp	Asp	Met	Tyr	Ser	Val	Leu
		35					40					45			
Pro	Glu	Asp	Arg	Ser	Gln	His	Leu	Gly	Glu	Glu	Leu	Gln	Gly	Phe	Trp
	50					55					60				
Asp	Lys	Glu	Val	Leu	Arg	Ala	Glu	Asn	Asp	Ala	Gln	Lys	Pro	Ser	Leu
65					70					75					80
Thr	Arg	Ala	Ile	Ile	Lys	Cys	Tyr	Trp	Lys	Ser	Tyr	Leu	Val	Leu	Gly
				85					90					95	
Ile	Phe	Thr	Leu	Ile	Glu	Glu	Ser	Ala	Lys	Val	Ile	Gln	Pro	Ile	Phe
			100					105					110		
Leu	Gly	Lys	Ile	Ile	Asn	Tyr	Phe	Glu	Asn	Tyr	Asp	Pro	Met	Asp	Ser
		115					120					125			
Val	Ala	Leu	Asn	Thr	Ala	Tyr	Ala	Tyr	Ala	Thr	Val	Leu	Thr	Phe	Cys
	130					135					140				
Thr	Leu	Ile	Leu	Ala	Ile	Leu	His	His	Leu	Tyr	Phe	Tyr	His	Val	Gln
145					150					155					160
Cys	Ala	Gly	Met	Arg	Leu	Arg	Val	Ala	Met	Cys	His	Met	Ile	Tyr	Arg
				165					170					175	
Lys	Ala	Leu	Arg	Leu	Ser	Asn	Met	Ala	Met	Gly	Lys	Thr	Thr	Thr	Gly
			180					185					190		
Gln	Ile	Val	Asn	Leu	Leu	Ser	Asn	Asp	Val	Asn	Lys	Phe	Asp	Gln	Val
		195					200					205			
Thr	Val	Phe	Leu	His	Phe	Leu	Trp	Ala	Gly	Pro	Leu	Gln	Ala	Ile	Ala
	210					215					220				
Val	Thr	Ala	Leu	Leu	Trp	Met	Glu	Ile	Gly	Ile	Ser	Cys	Leu	Ala	Gly
225					230					235					240
Met	Ala	Val	Leu	Ile	Ile	Leu	Leu	Pro	Leu	Gln	Ser	Cys	Phe	Gly	Lys
				245					250					255	
Leu	Phe	Ser	Ser	Leu	Arg	Ser	Lys	Thr	Ala	Thr	Phe	Thr	Asp	Ala	Arg
			260					265					270		
Ile	Arg	Thr	Met	Asn	Glu	Val	Ile	Thr	Gly	Ile	Arg	Ile	Ile	Lys	Met
		275					280					285			
Tyr	Ala	Trp	Glu	Lys	Ser	Phe	Ser	Asn	Leu	Ile	Thr	Asn	Leu	Arg	Lys
	290					295					300				
Lys	Glu	Ile	Ser	Lys	Ile	Leu	Arg	Ser	Ser	Cys	Leu	Arg	Gly	Met	Asn
305					310					315					320
Leu	Ala	Ser	Phe	Phe	Ser	Ala	Ser	Lys	Ile	Ile	Val	Phe	Val	Thr	Phe
				325					330					335	
Thr	Thr	Tyr	Val	Leu	Leu	Gly	Ser	Val	Ile	Thr	Ala	Ser	Arg	Val	Phe
			340					345					350		
Val	Ala	Val	Thr	Leu	Tyr	Gly	Ala	Val	Arg	Leu	Thr	Val	Thr	Leu	Phe
		355					360					365			

RAW SEQUENCE LISTING DATE: 06/18/2001
PATENT APPLICATION: US/09/647,140 TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt
Output Set: N:\CRF3\06182001\I647140.raw

```
163  Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg
164       370                 375                 380
165  Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg
166  385                 390                 395                 400
167  Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr
168                  405                 410                 415
169  Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser
170              420                 425                 430
171  Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly
172          435                 440                 445
173  Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro
174       450                 455                 460
175  Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln
176  465                 470                 475                 480
177  Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly
178                  485                 490                 495
179  Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala
180              500                 505                 510
181  Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile
182          515                 520                 525
183  Gly Asp Arg Gly Thr Pro Leu Ser Gly Gly Gln Lys Ala Arg Val Asn
184       530                 535                 540
185  Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp
186  545                 550                 555                 560
187  Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu
188                  565                 570                 575
190  Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
191              580                 585                 590
192  Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp
193          595                 600                 605
194  Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly
195       610                 615                 620
196  Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln
197  625                 630                 635                 640
198  Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
199                  645                 650                 655
200  Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
201              660                 665                 670
202  Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
203          675                 680                 685
204  Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
205       690                 695                 700
206  Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
207  705                 710                 715                 720
208  Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser
209                  725                 730                 735
210  Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly
211              740                 745                 750
212  Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr
```

<210> 9
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<400> 9
ctdgtdgcdg tdgtdggn 18

see item 9 on Error Summary Sheet

21

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 06/18/2001
PATENT APPLICATION: US/09/647,140 TIME: 16:26:36

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt
Output Set: N:\CRF3\06182001\I647140.raw

15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
1174 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
1174 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
1259 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
1259 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
1270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
1270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
1282 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
1282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
1282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18